

032301.218.seq.ST25.txt
SEQUENCE LISTING



<110> BATHE, Brigitte
<120> NUCLEOTIDE SEQUENCES WHICH CODE FOR THE *ppsk* GENE
<130> pA, sol WD 218
<160> 2
<170> Patentin version 3.1
<210> 1
<211> 1239
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (237)..(1022)
<223>

1400- 1
ggccgaagtt cctgcgaact attgcccata aaattcttcau ccaagatata tcttatacgtc 60
agccgatcga ctgtcgaact ttgtgtgttg gtg'agtcac acaaatttgtt gaggtcacaa 120
cgtttatccc tgatacgtac agcggtaagc gtggcagttt ccgcggcgat ggcacgcaac 180
tcattaaacg attgttgttc cataagacca tcacgttgtt tttttlagaa aattgc ctg 239
Met
1

cca aaa gcc gaa gta att tgt aca ctt ggg cgc atg act gag act gga 287
Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr Gly
5 10 15

ttt gga att gat atc ggt ggc tcc ggc atc aaa ggc gcc cgc gtt aac 335
Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val Asn
20 25 30

ctt aag acc ggt gag ttt att gat gaa cgc ata aaa atc gcc acc cct 383
Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr Pro
35 40 45

aag cca gca acc cca gag gct gtc gcc gaa gta gtc gca gag att att 431
Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile Ile
50 55 60 65

tct caa gcc gaa tgg gag ggt ccg gtc gga att acc ctg ccg tcc gtc 479
Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser Val
70 75 80

gtt cgc ggg cag atc gcg cta tcc gca gcc aac att gac aag tcc tgg 527
Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser Trp
85 90 95

atc gcc acc gat gtg cac gaa ctt ttt gac cgc cac cta aat gcc cga 575

Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly Arg
100 105 110

aac att acc att atc aat gac gca gar gcc gcc ggc atc gcc gaa gaa 623
Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu Ala
115 120 125

acc att gcc aac cct gcc gca cgc gaa gcc gca gtc atc ctg ctg acc 671
Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu Thr
130 135 140 145

ctt ggt aca gat att gga tcc gca ttc ctt gtg gat gat caa ctg ttc 719
Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu Phe
150 155 160

ccc aac aca gaa ctc ggt cgc atg atc gtt gac gcc gag gaa a a gaa 767
Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala Glu
165 170 175

cac ctt gca gca gca tcc gtc aaa gaa aac gaa gat ctg tca tgg aag 815
His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp Lys
180 185 190

aaa tgg gag aag cac ctg aac aag gtg ctg agc gaa tac gag aaa ctt 863
Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys Leu
195 200 205

ttc tcc cca tcc gtc ttc atc atc ggt gcc gga att tcc aga aag cac 911
Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys His
210 215 220 225

gaa aag tgg ctt cca ttg atg gag ata gac act gac att gtc cca gct 959
Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro Ala
230 235 240

gag ctg cgc aat cga gcc gga atc gta gga act gcc atg gca gta aac 1007
Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val Asn
245 250 255

caa cac ctc acc cca taagttatcg aaaggtgatt ttgcccagg gccttgattc 1062
Gln His Leu Thr Pro
260

acaacgcacc ttgctgtagg aaaaacaggc ccttttgtga catcgcgta gttgttcaac 1122

tataatggaa cgctgatcgt ggacaagagt taaccatgag attgattcac ccttttaagc 1132

ctccaaaagaa gtagttgact caacgcattt cggcatttaa aaaagccgag agcaaat 1239

<210> 2

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Met Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr
1 5 10 15

Gly Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val
 20 45 60

Asn Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr
 35 40 45

Pro Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile
 50 55 60

Ile Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser
 65 70 75 80

Val Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser
 85 90 95

Trp Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly
 100 105 110

Arg Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Ala Gly Ile Ala Glu
 115 120 125

Ala Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu
 130 135 140

Thr Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu
 145 150 155 160

Phe Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala
 165 170 175

Glu His Leu Ala Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp
 180 185 190

Lys Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys
 195 200 205

Leu Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Gly Ile Ser Arg Lys
 210 215 220

His Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro
 225 230 235 240

Ala Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val

032301.218.seq.ST25.txt

245

250

255

Asn Gln His Leu Thr Pro

260